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Controlling Avian Flu and Protecting People's Livelihoods in the Mekong Region

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Ducks, Rice and People - the Key to HPAI Risk in the Mekong Region

M. Gilbert, X. Xiao, D. Pfeiffer, M. Epprecht, S. Boles, C. Czarnecki, P. Chaitaweesub, W. Kalpravidh, P.Q. Minh, J. Otte, V. Martin and J. Slingenbergh

Key Findings

- HPAI risk in Thailand and Viet Nam is associated with duck abundance, human population and rice cropping intensity but poorly associates with chicken numbers.
- A statistical model of the spatial risk of HPAI occurrence derived from one epidemic wave in Thailand maintained its predictive power when applied to Viet Nam.
- The model can thus be used for spatial prediction of the risk of HPAI in other countries with similar agro-ecological conditions.

Thailand and Viet Nam have both experienced several epidemic waves of HPAI H5N1 between 2004 and 2005. The situation in the two countries is particularly interesting to compare because they applied different control strategies, succeeded in temporarily controlling the virus, and faced periodic re-occurrences (Figure 1). Viet Nam undertook massive, repeated vaccination campaigns in combination with other control measures. Thailand has not applied vaccination and placed emphasis on early detection, prevention of poultry movements in high risk areas, including pre-movement testing, and transformation of the free-ranging duck production sector. It is difficult to assess whether the re-occurrences experienced by both countries resulted from local persistence of the virus or from new introductions, but recent results suggest that Southeast Asia may constitute a regional 'evolutionary sink' for HPAI H5N1 virus, supporting the notion that the region faces periodic re-introductions.

Duck, Rice, People and HPAI H5N1

Spatial and temporal patterns of these HPAI waves in each of the two countries has been presented and discussed in detail in previous scientific papers. However, the data had never been analyzed simultaneously for the two countries using a common set of risk factors (elevation, human population, chicken and duck density) in an attempt to identify common features of the different epidemics in time and space. Although the epidemics had different spatial patterns in the two countries (Figure 2), considerable consistency was found across the waves and countries in the statistical association between HPAI H5N1 virus presence and selected risk factors. The variables showing the highest level of consistency in their relationship with HPAI H5N1 virus presence were *human population*, *rice cropping intensity*, and, to a somewhat lesser extent, *duck numbers*, all of which were significantly associated with virus presence in both countries. Chicken numbers failed to be identified as a significant predictor of disease presence, except in wave-III in Viet Nam. The latter is probably due to the fact that wave-III primarily affected the Red River delta where chickens are far more dominant than in the rest of the country.

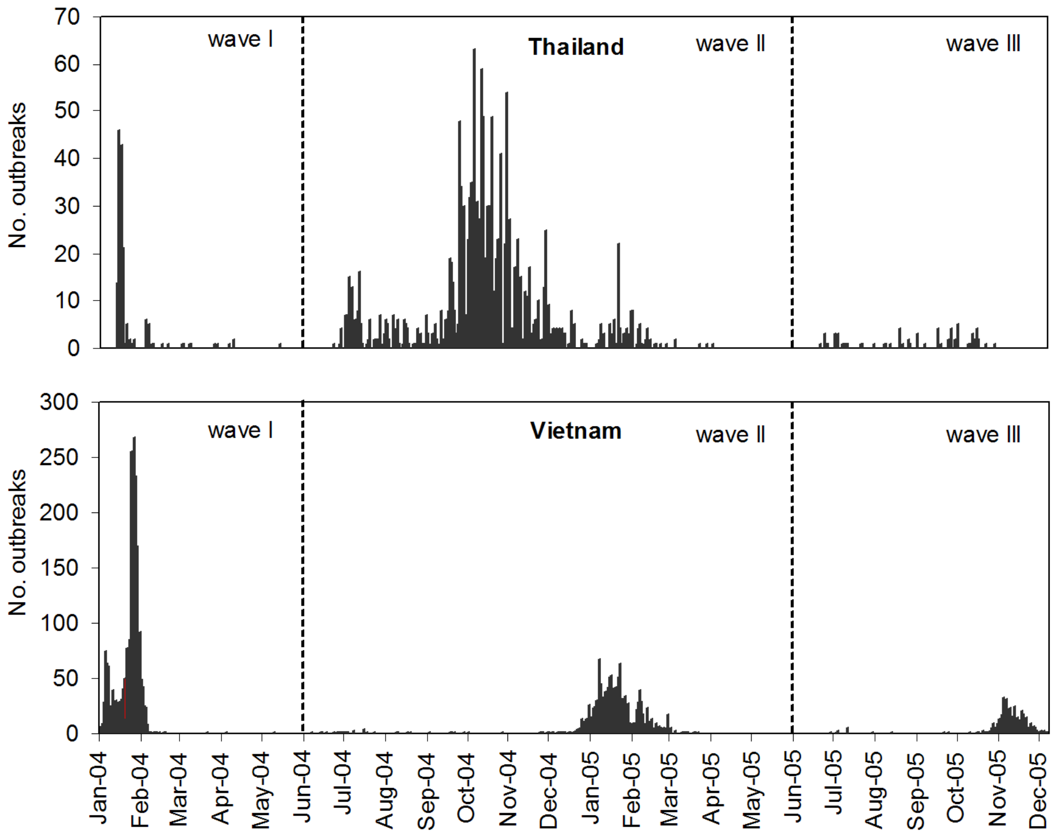

Figure 1. Temporal distribution of daily HPAI H5N1 virus records reported in Thailand and Viet Nam.

Mapping the Risk of HPAI H5N1 Presence in the Region

Although the statistical model based on those three variables only had a moderate predictive power, the predictions appeared to be relatively robust. This was tested by evaluating the performance of a model based on Thailand wave-II data in its ability to predict the presence of HPAI H5N1 in Viet Nam (waves-I, II and III) and Thailand (waves-I, and III). The predictive power of the Thailand wave-II model was very close to that of each wave's best-fit model, as measured by their respective areas under the curve of the receiver-operating characteristic plots. This validation exercise showed that the model maintained its predictive power when extrapolated in time and space, and thus an equivalent predictive power can be expected when applying it to other countries sharing similar agro-ecological conditions, such as Lao PDR or Cambodia. This feature allowed the generation of a general HPAI risk map for the Mekong countries (Figure 3).

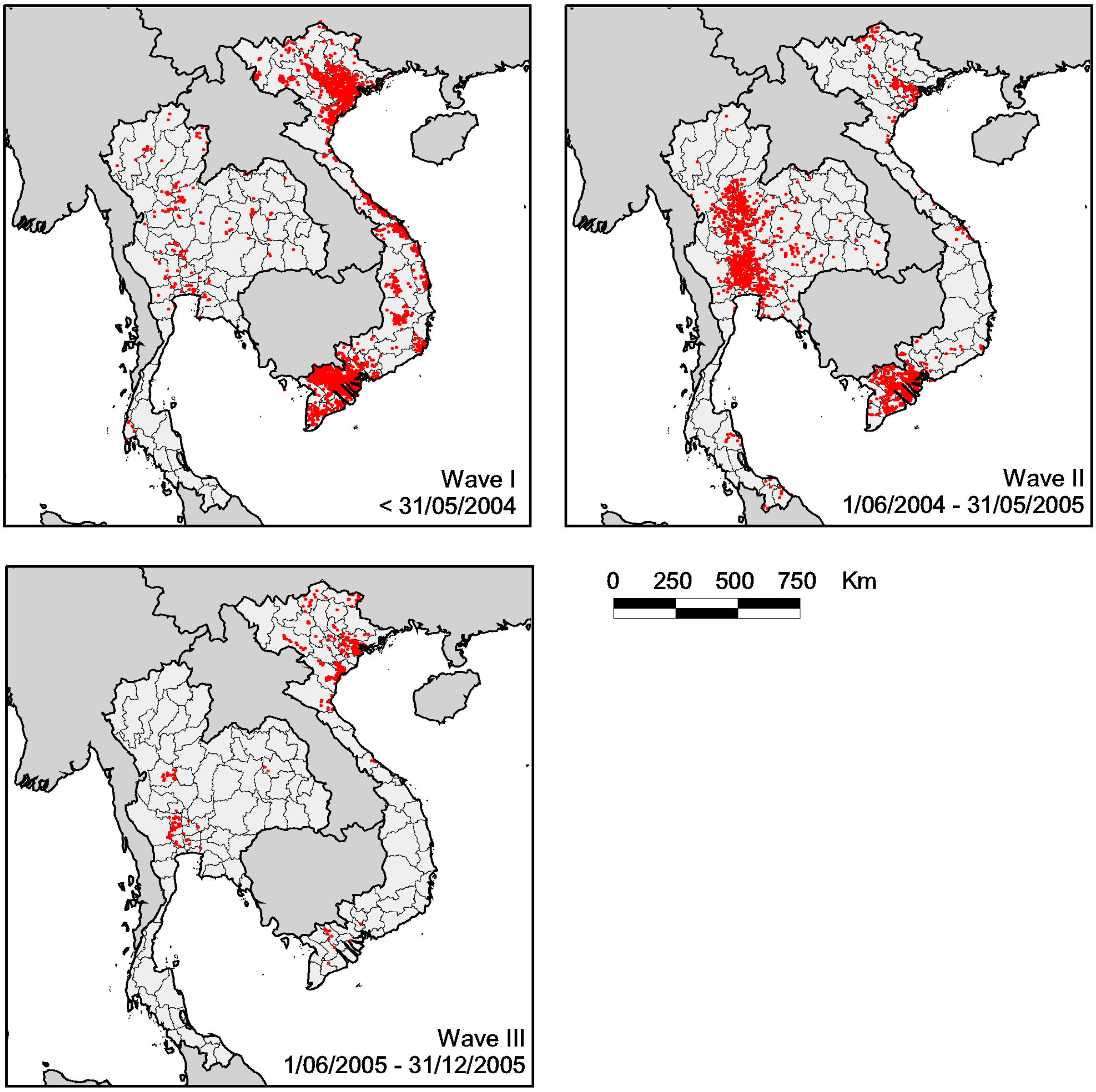

Figure 2. Spatial distribution of HPAI H5N1 virus records reported during the three main epidemic waves in Thailand and Viet Nam.

Future Work

Considerable variation remained unexplained by the model, and HPAI disease risk should be considered in conjunction with other factors such as the production systems for terrestrial poultry, wet markets, potential for contacts with migratory and resident avifauna, and conditions affecting persistence of the virus in the environment.

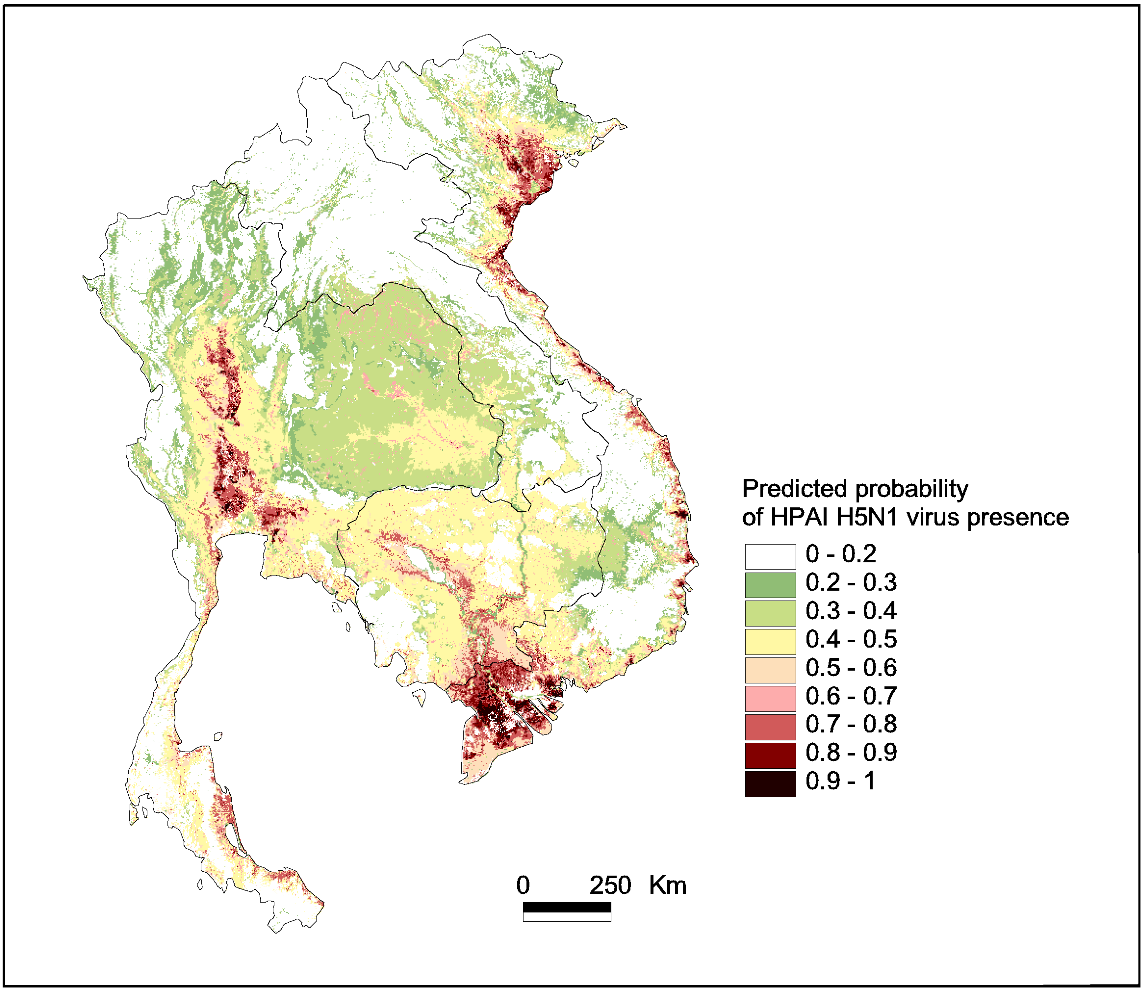

Figure 3. Predictions of HPAI H5N1 virus relative risk of presence in Thailand, Lao PDR, Cambodia, and Viet Nam based on the Thailand wave-II model

A striking feature of the different epidemic waves displayed in Figure 1 is that they do not appear to be synchronous, which raises questions about the underlying factors that may define ‘hot’ periods during which increased virus circulation can be expected. Thus, whilst the capacity to define the risk of HPAI H5N1 virus circulation in the spatial domain has improved, understanding the factors related to high disease risk in the temporal domain is still elusive. Preliminary work suggests that much could learned in that regard from the comparative analysis of the seasonality of the duck and rice production, climatic conditions, and HPAI in different countries.

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